



REPLACEMENT SHEET

1/13

The intron sequences between exons 2 - 3 and exons 18 - 19 are missing (introns: small letters, exons: capital letters). Small letters in the first exon indicate nucleotides that have not been unambiguously determined.

Exon 1

```
1  CGGGTGAATC CCGGCGCCGC GCCCCGGACC CGCAGCTCCC TGCCTCCTC
51  CCTCCCAGCC GCTTTAACAC CCACACCCCA CAGTCTCTCC CACGsCCGCG
101 CCTTGGCGGC CCCACTGAAT CCCTACGCGG GGCCCAGCGG TACCGGGAGA
151 CCGGGCTAGC CTATGGGAGC GCCCAGATAA CGCGGGTTGG GGGCGCCCCG
201 GCCCCcATCC CCGCCAGCAT GACTCGATCG CCGCCCCCTCA GAGAGCTGCC
251 CCCGAGTTAC ACACCCCCAG CTCGAACCGC AGCACCCCAG gtgagtagag
301 ggggagctgg aagaagggaag agagcggagc caggtctgtc actcgggcct
351 ctgcaagggtt tgtgatgtct tgaagtgccg agtgtcatta gatgtctgaa
401 ggcaagttag agccagcacc gcaagcaagt tgtgcgtgtg tgtcgggtgtg
451 tctgtgccgg tgtctcctca tcgtctggcc agtgagaatg aatgtctgtg
501 gggtcacctc tgtgtccacc cgacgacagg tgtgtgtaca tatgtatcct
551 gctctcagaa aatgggccta tgccgccggg cgcggtgact cagcctgta
601 atcccaacac tgggagggtg aggcaggcag attacctgag gtcaggagtt
651 cgagaccagc caggccaaca tggggaaact ctgtctctac taaaaataaa
701 aattagcagg gcgtgggtggc gggcgccctgt agtcccaact actcgggagg
751 ctgaggcagg agaattctctt gaacctggga ggcggagggtt gcagtcaagc
801 cgagatcaca ccactgcact ccagccaggg caacagagcg agatgcgtct
851 caaaaaaaaa aaaaaaaaaa aaaaggagag aaaacaaaaa gaaaagaaag
901 gaaaataggc ctatgccttc ctcagggtgtg tgctggggat ggtgggtgtt
951 acatcttcca agtctgggcc tgtgtctgtg ttggtgctcc ctgtcccaca
1001 tccagaaatc aagaagcgag ggctgggcag cagatatata gggtgagaag
```

Fig.1A



REPLACEMENT SHEET

2/13

1051 ggaaggattt catgcattgt tacagtgatg cctggctgac ccttctcttt
EXON 2
1101 ccatcccagA TCCTAGCTGG GAGCCTGAAG GCTCCACTCT GGCTTCGTGC
1151 TTA CTTCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT
1201 GTGGCAAAGT GCTCTTTCTG GGACTGTTGG CCTTTGGGGC CCTGGCATT
1251 GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA
1301 AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA TTACACCAAG GAGAAGCTGG
1351 GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG
1401 GAGGGAGAGA ACATCCTCAC ACCCGAAGCA CTTGGCCTCC ACCTCCAGGC
1451 AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAG.....
1501g
1551 tgagtctggc tgagcccctg agcagctggg ggcgaggcgt gctgtggggg
1601 ttctggagtg ggaatcccct tcttctgctg atctcctatg cccctggcta
EXON 4
1651 ttgcagTCCT GGGATTTGAA CAAAATCTGC TACAAGTCAG GAGTCCCCCT
1701 TATTGAAAAT GGAATGATTG AGCGGgtaag tgtcctgaga gggagtagag
1751 gcagaacttt ttctgtagcg tgggaggact cagagaccga gcaagcccca
1801 cagcctgcaa tctgccccct taaaactaag gagggggatt gcagagggca
1851 tcctacaaag gttgtggggc aggactgacg tggcccgggg tatccctggc
EXON 5
1901 agATGATTGA GAAGCTGTTT CCGTGCGTGA TCCTCACCCC CCTCGACTGC
1951 TTCTGGGAGG GAGCCAAACT CCAAGGGGGC TCCGCCTACC TGCCgtgagt
2001 gccactcctg gggccctgct tcatctcccg ctggggactc tcccagcaga
2051 aaggaggggt ctggggaatg aggatgatca aaaccttacc aaggtcctaa
2101 ttacctcca gcccaggaac agagagcatg ggcttcccca aggtctctct
2151 cacatcctcc ttctcttctc ctctcaagga aggaagacct gacttattta
2201 cacaaaacta aacacaaaga tctgtaagat ctgagcaaag gagaaaaaga
2251 tccccacaaa gaggctttgc tgggggaaat tacctaggtg tttgctaagc
2301 cattgcccag gccagaaaga aaacctgcta caggcatgtg cctgctgggt
2351 gtatattaga accaagcaca cagcttggtg aggaactcag tggggccttt

Fig.1B



REPLACEMENT SHEET

3/13

2401 ctgggccctt tctatgtatt aggtaaccct gccctgatat tcgtctcagc
2451 cccttgtagt cttctacagc tctactgtagc accctgggtgg gcccatgcag
2501 cctggcagtt ctgagaagct gaggcttgca caccctccat atggaaggac
2551 aaatcggcag ataagaggag ggtgggggtac agcatggcgc cccagcagca
2601 gtttgagacc tgggttttcg tccctgaccc tcaccaacta taggcttttc
EXON 6
2651 cctcagCGGC CGCCCGGATA TCCAGTGGAC CAACCTGGAT CCAGAGCAGC
2701 TGCTGGAGGA GCTGGGTCCC TTTGCCCTCCC TTGAGGGCTT CCGGGAGCTG
2751 CTAGACAAGG CACAGGTGGG CCAGGCCTAC GTGGGGCGGC CCTGTCTGCA
2801 CCCTGATGAC CTCCACTGCC CACCTAGTGC CCCCACCAT CACAGCAGGC
2851 AGgtgggttc caaccaggtc tgccagggaa aggetgtttt ccttcccttt
2901 cccttctca tactcctgtg ttctggggga gctgactgct ctgtgccctg
2951 acccccccact tcctggccat tattaccctg ctcccacagt gccaggcccc
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3251 tattagcctc ccaaagtgt gggattacag gcgtgagcca ctgcgcctgg
3301 ccaaggctgg actttttatc aaaatagact aatacaggga aactaagaac
3351 acagcaggta agcatgaata tcatacctgg tttcccaggt ttctttgtgg
3401 ccctgcaaat gtggtacttt ttccagaatc cgccagttac accagctcct
3451 cccagaagcc tacttccagg cctctgcttc cccttggggc ttctgtctg
3501 cgggatacta gctgttctact cctgcagagc agtcaagagg ctcaagaatag
3551 ttacctacac tccagcccta ctgagcttca tggcagcgtg gttcctggag
3601 gtggaagccc agggacactc agttatccac ggccagggcc ttgagcatta
EXON 7
3651 acccctcctg ttcccctcca gGGCTCCCAA TGTGGCTCAC GAGCTGAGTG
3701 GGGGCTGCCA TGGCTTCTCC CACAAATTCA TGCCTGGCA GGAGGAATTG

Fig.1C



REPLACEMENT SHEET

4/13

3751 CTGCTGGGAG GCATGGCCAG AGACCCCCAA GGAGAGCTGC TGAGgtaggg
3801 tctcctctgg gagttggtga ggggactctg ttcattgagaa cccatactgt
3851 aatgccaggc agctctggca aaaggccctt cacatccctc accaggtggt
3901 tgggccagct ctgaccctg gttctccac acccccacca gGGCAGAGGC
3951 CCTGCAGAGC ACCTTCTTGC TGATGAGTCC CCGCCAGCTG TACGAGCATT
4001 TCCGGGGTGA CTATCAGACA CATGACATTG GCTGGAGTGA GGAGCAGGCC
4051 AGCACAGTGC TACAAGCCTG GCAGCGGCGC TTTGTGCAGg tgggtatgga
4101 caaggacaag gggggtgccc tgaggccatt ccctcctcct gccccctcct
4151 atccaccctg tttctccagC TGGCCCAGGA GGCCCTGCCT GAGAACGCTT
4201 CCCAGCAGAT CCATGCCTTC TCCTCCACCA CCCTGGATGA CATCCTGCAT
4251 GCGTTCTCTG AAGTCAGTGC TGCCCGTGTG GTGGGAGGCT ATCTGCTCAT
4301 Ggtgggtctt gcacctggca ccttgcccc accccacctc caaccagtgc
4351 ccaccctggg agccctgag actgccctt cccccacag CTGGCCTATG
4401 CCTGTGTGAC CATGCTGCGG TGGGACTGCG CCCAGTCCCA GGGTTCCTG
4451 GGCCTTGCCG GGGTACTGCT GGTGGCCCTG GCGGTGGCCT CAGGCCTTGG
4501 GCTCTGTGCC CTGCTCGGCA TCACCTTCAA TGCTGCCACT ACCCAGgtac
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4651 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT
4701 CTGCCTGGCA CCCCTCTCCA Ggtggggcct tgtccccag ggctcatctg
4751 aggcagctca gcttactggt taagagcctc ttggttcaag tgacccttgg
4801 gctgctaatag aacctcggtg cctcttgtcc ccatctgtaa acaggggaaa
4851 taatagtget gtgtcctaag gggtattggt tggatcagtg aggttaactca
4901 agttgaatgc ttagaacagc ccatcatagc tacatggtac ccaataaatg
4951 ctagccactg tggtatgact gccccacctc tgcaccccaa gttcctgagc
5001 ctcccccttca ctccactttg acacggcccc tcccttgtga cctgagggca
5051 ggtccccact ctgtcctggc agGAGCGCAT GGGCGAGTGT CTGCAGCGCA

Fig.1D



REPLACEMENT SHEET

5/13

5101 CGGGCACCAG TGTCGTACTC ACATCCATCA ACAACATGGC CGCCTTCCTC
5151 ATGGCTGCCC TCGTTCCCAT CCCTGCGCTG CGAGCCTTCT CCCTACAGGC
5201 GGCCATAGTG GTTGGCTGCA CCTTTGTAGC CGTGATGCTT GTCTTCCCAG
5251 CCATCCTCAG CCTGGACCTA CGGCGGCGCC ACTGCCAGCG CCTTGATGTG
5301 CTCTGCTGCT TCTCCAGgta ctgcggtgcgc cccagccccct tcctcccgtg
5351 acccacgcca gcctgtcccc tcaccagcat ttcaaggcac agacctgtca
EXON 13
5401 tccactctct acctcttcca gTCCCTGCTC TGCTCAGGTG ATTACAGATCC
5451 TGCCCCAGGA GCTGGGGGAC GGGACAGTAC CAGTGGGCAT TGCCCCACCTC
5501 ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT
5551 GGTCACCATC CTGCCTCCCC AAGCCACCT GGTGCCCCCA CCTTCTGACC
5601 CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA
5651 GGCCAGGAGG AGGAGACAAG GCAGAAGGCA GCCTGCAAGT CCCTGCCCCG
5701 TGCCCCGCTGG AATCTTGCCC ATTTGCCCCG CTATCAGTTT GCCCCGTTGC
5751 TGCTCCAGTC ACATGCTAAG gtaagactgg gcagagcagg gcagagactt
5801 agcatctctg ggcccagaag ggcagagagg gcttagtcca ctgcctgagg
EX
5851 ggctgggggc agccctgggg tctccagctt agttgctaca tcccgcagGC
XON 14
5901 CATCGTGCTG GTGCTCTTTG GTGCTCTTCT GGGCCTGAGC CTCTACGGAG
5951 CCACCTTGGT GCAAGACGGC CTGGCCCTGA CGGATGTGGT GCCTCGGGGC
6001 ACCAAGGAGC ATGCCTTCCT GAGCGCCCAG CTCAGGTACT TCTCCCTGTA
6051 CGAGGTGGCC CTGGTGACCC AGGGTGGCTT TGA CTACGCC CACTCCCAAC
6101 GCGCCCTCTT TGATCTGCAC CAGCGCTTCA GTTCCCTCAA GGCGGTGCTG
6151 CCCCCACCGG CCACCCAGGC ACCCCGCACC TGGCTGCACT ATTACCGCAA
6201 CTGGCTACAG Ggtgagaggc gaggagacgg gcagggaggg gtgctgcagg
6251 gagaaacgcc ctgggggccac cagctaataa aaccctatcc tgggtctcccc
EXON 15
6301 cagGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGCATCACC
6351 CGCCACTCGA CCGCAATGGC TCTGAGGATG GGGCCCTGGC CTACAAGCTG
6401 CTCATCCAGA CTGGAGACGC CCAGGAGCTT CTGGATTTC GCCAGgttgg

Fig.1E



REPLACEMENT SHEET

6/13

6451 gagagggctg gaggggtcca ctagtacagg ggctgcaggc ctcctgggcc
EXON 16
6501 caggccttca gccctctctg cctctgcagC TGACCACAAG GAAGCTGGTG
6551 GACAGAGAGG GACTGATTCC ACCCGAGCTC TTCTACATGG GGCTGACCGT
6601 GTGGGTGAGC AGTGACCCCC TGGGTCTGGC AGCCTCACAG GCCAACTTCT
6651 ACCCCCCACC TCCTGAATGG CTGCACGACA AATACGACAC CACGGGGGAG
6701 AACTTTCGCA gtgagtcttg gggggagctc ggcaagagcc tcagcctcgc
6751 ccacacaagc cctgagcctg aggccctgcc cactctgccc cgtgctcacc
EXON 17
6801 gccctgtccc tctccctctt ctcccttccc ctccctcca cagTCCCGCC
6851 AGCTCAGCCC TTGGAGTTTG CCCAGTTCCC TTTCTGCTG CGTGGCCTCC
6901 AGAAGACTGC AGACTTTGTG GAGGCCATCG AGGGGGCCCG GGCAGCATGC
6951 GCAGAGGCCG GCCAGGCTGG GGTGCACGCC TACCCAGCG GCTCCCCCTT
7001 CCTCTTCTGG GAACAGTATC TGGGCCTGCG GCGCTGCTTC CTGCTGGCCG
7051 TCTGCATCCT GCTGGTGTGC ACTTTCCTCG TCTGTGCTCT GCTGCTCCTC
7101 AACCCTGGA CGGCTGGCCT CATAgtgagt gcttgcagga gtggggacag
7151 agacacccca cccttcctg cccagcctgt catccctcct gccaggagcc
EXON 18
7201 ctctgtgagc cctgtctccc tcagGTGCTG GTCCTGGCGA TGATGACAGT
7251 GGAACCTTTT GGTATCATGG GTTTCCTGGG CATCAAGCTG AGTGCCATCC
7301 CCGTGGTGAT CCTTGTGGCC TCTGTAGGCA TTGGCGTTGA GTTCACAGTC
7351 CACGTGGCTC TGGGCTTCCT GACCACCCAG GGCAGCCGGA ACCTGCGGGC
7401 CGCCCATGCC CTTGAGCACA CATTTGCCCC CGTGACCGAT GGGGCCATCT
7451 CCACATTGCT GGGTCTGCTC ATGCTTGCTG GTTCCCATT TGAATTATT
7501 GTAAG.....
7551 gtagggaggg ctcggggcag ggaggcagg ctcaggacag
EXON 20
7601 gcctgggctg actccccca caccctaccc ctagGTACTT CTTTGC GGCG
7651 CTGACAGTGC TCACGCTCCT GGGCCTCCTC CATGGACTCG TGCTGCTGCC
7701 TGTGCTGCTG TCCATCCTGG GCCCGCCGCC AGAGgtgacc acaccctcgg
7751 caccatccct ctactcccag cccaaggagac ggggtaggga gaggcaagg

Fig.1F



REPLACEMENT SHEET

7/13

7801 aagggacaga gccctgtggc ccacagacag gtacctcccc aacaggtgcc
7851 accagctgaa ggtggcagcc tcctcctttc ccagacacc atgttcctgc
7901 ccctcagccc tcctggttc ttcattgggac ccaccttaga ctttttaggat
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8001 cagctctcat atcctgctgg agaccaacaa gggccccagc ttcccaacag
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8151 GGAAAGCCCA GAGATCCTGA GTCCACCAGC TCCACAGGGA GCGGGGCTTA
8201 Ggtggggggc atcctcctcc ctgccccaga gctttgccag agtgactacc
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9051 ccaggacctg aggtattagc ttctctagtt ctgggtggaa aagacccccg
9101 attctggatt tttgtcatat acttggtaac atcatctgga ttaagtgcct

Fig.1G



REPLACEMENT SHEET

8/13

9151 actatacaaa acgataacaa attttgttgg tgtgaaatcc tactgggttc
9201 aatctggaga ccgagagcag aaaaaaaga accccactgt gtggctttca
9251 gagccaccat attccagcct gcccgctctct ccagactcac ctccacctac
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9351 caggtggaag gcgaggtgga ggcagatcag gaaagcagcc agttgaagca
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10101 atagtgcaa gggggtcagc cctcagtgcc acttaccagc ggagtaacc^E
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XON 22
10201 CCCGAGGAGA Tc**TAG**CCTCT GCCTCCCACC CCAGCACCCC CTCATCAGAC
10251 ACAAGGAGCG CCACTGTCTG GACAGGCTGA ATTGGTCTTC GGGTCCCTAA
10301 TTTCTCATAC GCCATTCCCT CTGCCTAGAA CACTTTCTCA CCTCCCCTTG
10351 ATGTGACCCC ATATCACCT TCGAGGTGAA TTGGATCGGA TGCCATCTCC
10401 TCCAGGAGGG GTGGGGTCGT GCCTCCTGTG AGGTCCCAGT GCCCCTGAGT
10451 GTCTGTGCCC GTCTGTTTCC CCGTCCCTCT CTCTAAGCCC GGAGGCTTAC

Fig.1H



REPLACEMENT SHEET

9/13

10501 TCGGGTAAG GACGGCGGGA CAGGACCTTA ACCCCTGGGA CGAACACCAG
10551 CTCCGCAAAG GACTCCGCAC CCGGCGCCGC CCACGGGGTG CGGGTCCCAG
10601 GAGGACCAGC AGAGAGGAGC ATAGGAGAGC AAAGGAGATC AGTGACCCAT
10651 GGCTTCCCCG GTGGCGCGGA ACAGCCCGGA GCCGCCTGTG ATTTGCATAC
10701 CCATGGTGCA CCACGAAAAG ATACCCTCAA GATGCTTGCA CTCCCTCTGT
10751 GCGCGCATTT CTGCACTGTT TTAGAGCATG ATGCCTCTTA CACGCATCTG
10801 TGTGCATAAA CTACATATAG GGAGTGCCTA CCACGCAGGC ATCCAACAAC
10851 CATAAGTGTG TTAAGTGTTA GTTCTCCCTG CGAGGTTCGA AGCGGAAGTC
10901 ACGAATATAC TCGGGTTTCT CTTCAAAGCG CATAAATCTT TCGCCTTTTA
10951 CTAAAGATTT CCGTGGAGAG AAAGTTGTGA GTTTTTATTTC AATTTTTTGA
11001 GGCCTCTTAT TTCCTGAGGC TACATTTTTA AGTATTAAAA GTTAGGCAAC
11051 TACAAAAAAA AAAAAAAA

Fig.1I



REPLACEMENT SHEET

10/13

1MTRSPPLRELP..... 11
1 MASAGNAAEPQDRGGGSGCIGAPGRPAGGGRRRRTGGLRRRAAPDRDYL 50
12 ..PSYTPPARTAAPQI...LAGSLKAPLWLRAYFQGLLFSLGCGIQRHCG 56
51 HRPSYCDAA.FALEQISKGKATGRKAPLWLRKAFQRLLFKLGCIYQKNCG 99
57 KVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRSVSELHYTKEKLG 106
100 KFLVVGLLIFGAFVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGE 149
107 EAAYTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDL 156
150 EAMFNPQLMIQTPKEEGANVLTTEALLQHLDLSALQASRVHVYMYNRQWKL 199
157 NKICYKSGVPLIENGMIERMIEKLFPCVILTPLDLFWEGAKLQGG SAYLP 206
200 EHLCYKSGELITETGYMDQIEYLYPCLIIITPLDLFWEGAKLQSGTAYLL 249
207 GRPDIQWTNLDPEQLLEELGPFA.SLEGFRELLDKAQVGQAYVGRPCLHP 255
250 GKPLLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGYMDRPLNP 299
256 DDLHCPPSAPNHHSRQAPNVAHELSGGCHGF SHKFMHWQEELLLGGMARD 305
300 ADPDCPATAPNKNSTKPLDMALVLNNGGCHGLSRKYMHWQEELIVGGTVKN 349
306 PQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAW 355
350 STGKLVSahalQTMFQlMTPKQMYEHFKGYEVSHINWNEDKAAAILEAW 399
356 ORRFVQLAQEALPENASQQIHAFSSTLDDILHAFSEVSAARVVGGYLLM 405
400 QRTYVEVVHQSV AQNSTQKVLSTTTTLLDDILKSFSVSVIRVASGYLLM 449
406 LAYACVTMLRWDCAQSQSGVGLAGVLLVALAVASGLGLCALLGITFNAAT 455
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456 TQVLPFLALGIGVDDVFLLAHAFTEALPG..TPLQERMGECLQRTGTSVV 503
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504 LTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLD 553
550 LTSISNVTAFFMAALIPIPALRAFSLQA AVVVVFNFAMVLLIFPAILSM D 599
554 LRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGT.....VPVG 592
600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHS 649
593 IAH.....LTATVQAFTHCEASSQHVVITILPPQAHL....VPPPSDPLGS 633
650 FAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSC 699

Fig.2A



REPLACEMENT SHEET

11/13

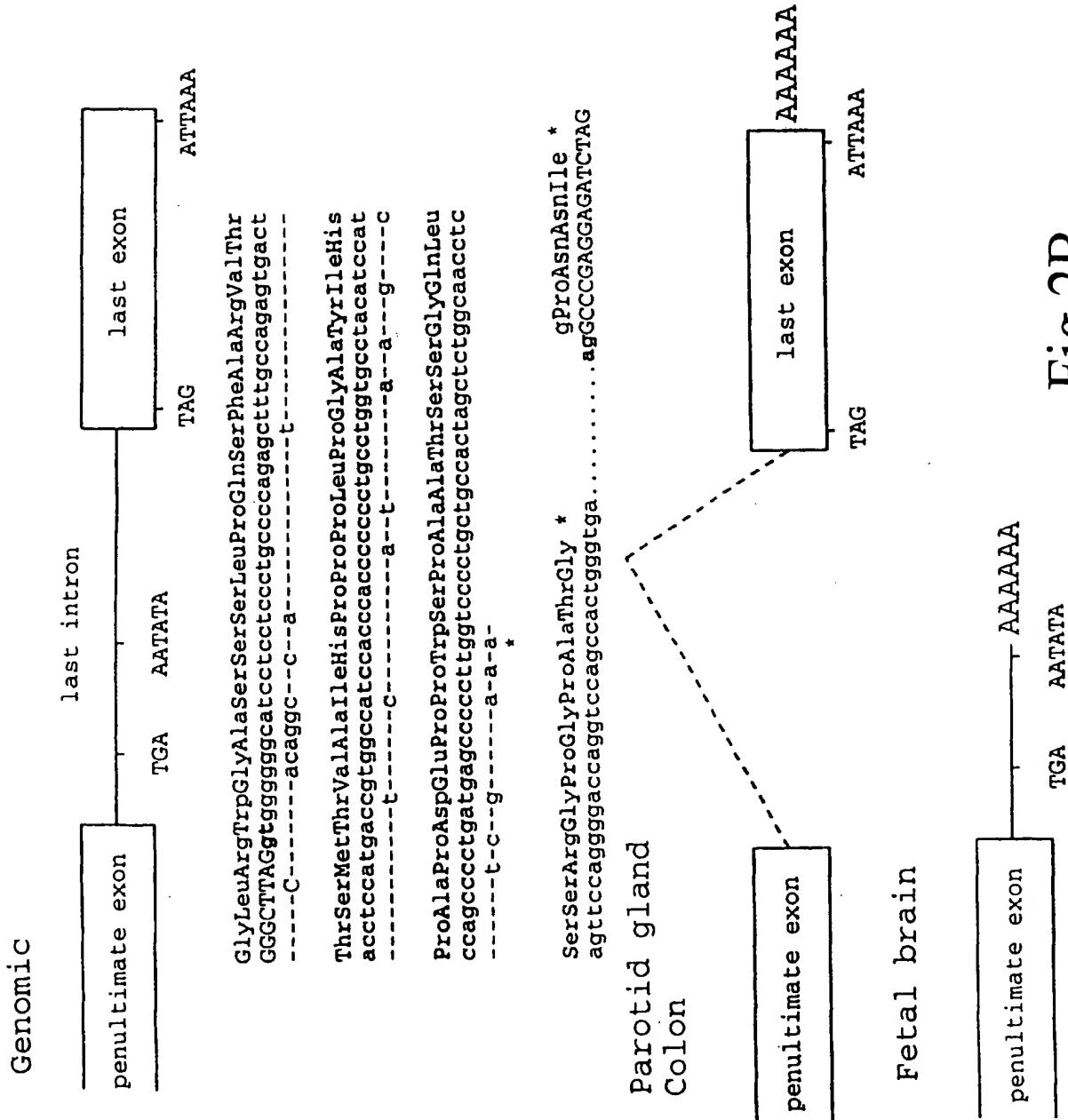
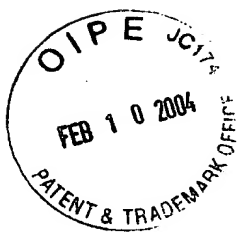


Fig.2B



REPLACEMENT SHEET

12/13

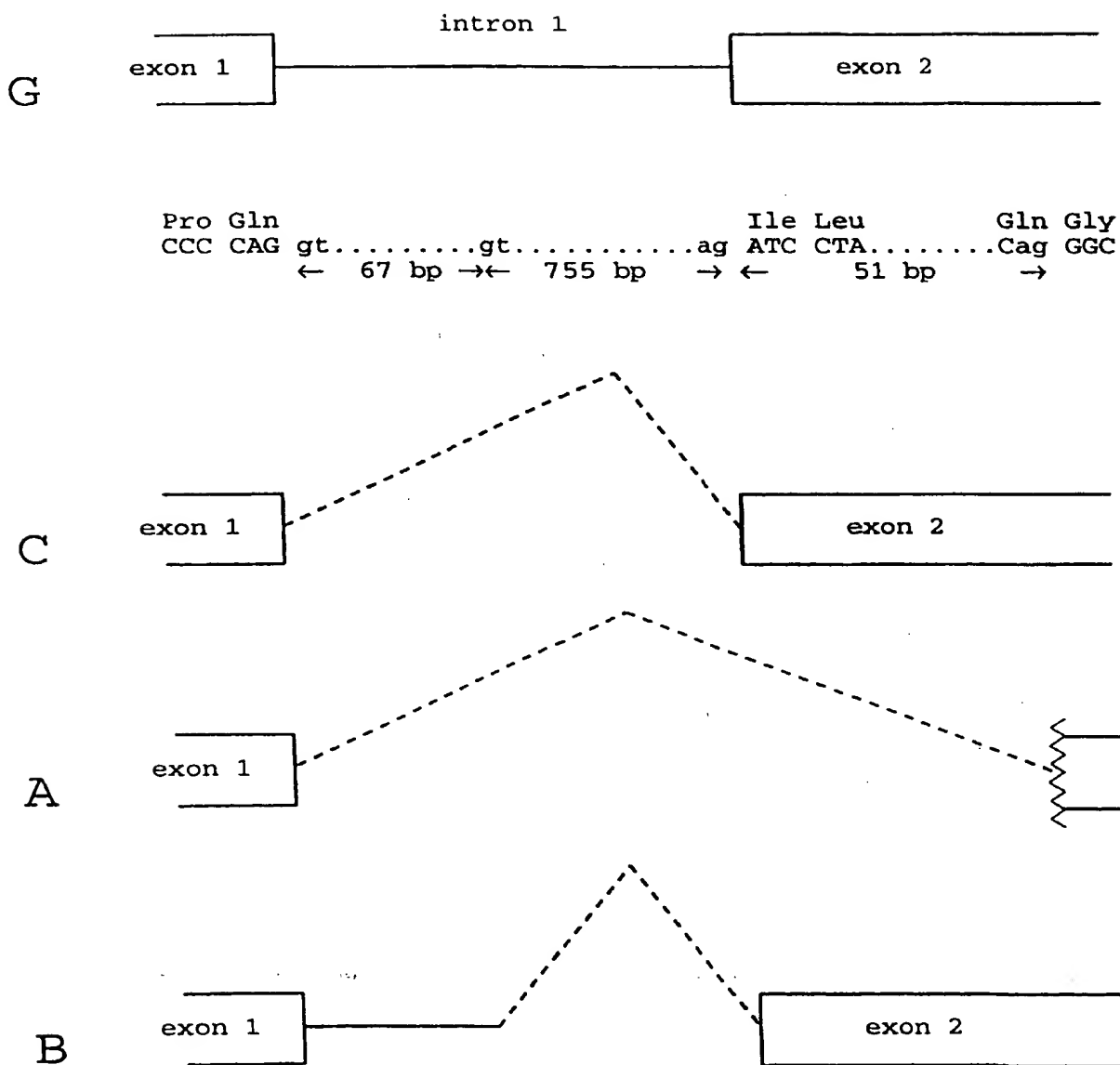


Fig.2C

REPLACEMENT SHEET

13/13

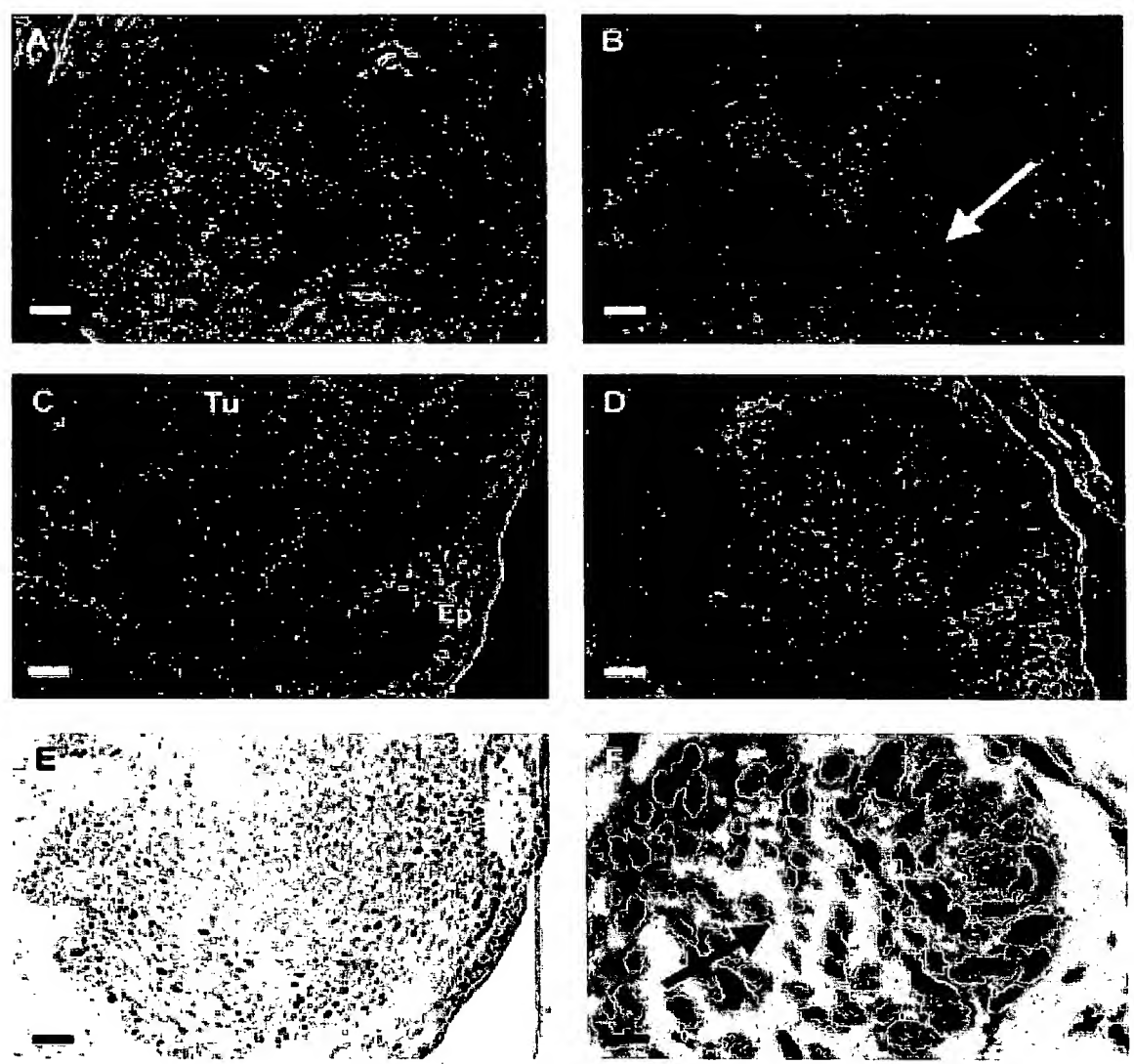


Fig.3